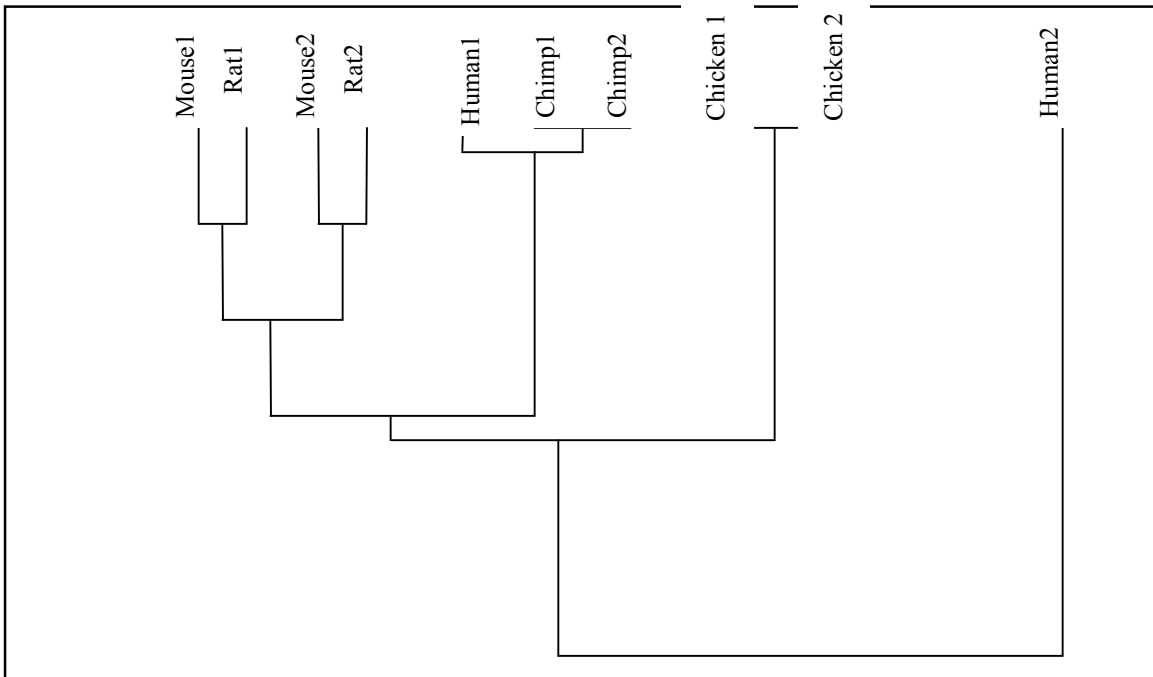


Quiz 1 Redo
(Take home question due Sunday is worth 30 points)

1. Describe how the phylogenetic analysis of HIV contributed to an understanding of the evolution of its virulence in humans. (15 points)

2. A molecular biologist friend of yours is interested in studying variation in a particular gene across a variety of vertebrates. She develops PCR primers to amplify the entire gene, based on sequence similarities at the 5' and 3' ends (i.e., start and finish) of the gene sequence in *C. elegans* and mice. She then uses these primers to sequence the gene from two mice, two rats, two humans, two chimps and two chickens. She aligns the sequences and creates a tree of gene relationships which looks like this:



Assume the branch lengths on the tree (the vertical dimension) are proportional to the number of sequence differences, and there have been no lab errors (i.e., the sequences actually came from the subjects and not from a contaminant). What hypotheses would you suggest to your friend to explain her results? How could she test these hypotheses with just the sequence information? (20 points)

3. A population geneticist studying a natural population of a beetle species has discovered variation in the exoskeleton structure. In a survey, she finds a 3:1 ratio of dull to shiny exoskeletons. Assuming that this phenotypic variation is caused by two alleles at a single locus, can the geneticist conclude that the *dull* allele is dominant to the *shiny* allele? Explain your answer. (15 points)

4. In a survey of protein variation (allozymes), the population geneticist samples from several different populations of these beetles and finds two alleles at the esterase (Est) locus, which she designates Est-1 and Est-2. In all the populations the frequency of Est-1 and Est-2 are each 0.5. Describe two alternative hypotheses to explain why the frequencies are the same in all populations, and propose experimental or observational studies that would test your hypotheses. (20 points)